RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/840,277C_

Source: _IFw/6_

Date Processed by STIC: _6/21/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):**
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _O9/840,277C_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
        Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
        Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
     ensure your subsequent submission is saved in ASCII text.

15 (maybe more)

5 ✓ Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
     each n or Xaa can only represent a single residue. Please present the maximum number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
        "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
        (NEW RULES)   <210> sequence id number
     <400> sequence id number
     000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
        Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
     is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
        "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFW16

```
 3 <110> APPLICANT: FEIGE, ULRICH
 4        KOHNO, TADAHIKO
 5        LACEY, DAVID
 6        BOONE, THOMAS CHARLES
 8 <120> TITLE OF INVENTION: ADHESION ANTAGONISTS (as amended)
10 <130> FILE REFERENCE: A-688A
12 <140> CURRENT APPLICATION NUMBER: US 09/840,277C
13 <141> CURRENT FILING DATE: 2001-04-23
15 <150> PRIOR APPLICATION NUMBER: US 60/198,919
16 <151> PRIOR FILING DATE: 2000-04-21
18 <150> PRIOR APPLICATION NUMBER: US 60/201,394
19 <151> PRIOR FILING DATE: 2000-05-03
21 <160> NUMBER OF SEQ ID NOS: 137
23 <170> SOFTWARE: PatentIn version 3.2
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 684
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(684)
35 <400> SEQUENCE: 1
36 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg      48
37 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
38 1               5                   10                  15
40 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      96
41 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
42             20                  25                  30
44 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc     144
45 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
46             35                  40                  45
48 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag     192
49 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
50     50                  55                  60
52 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg     240
53 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
54 65                  70                  75                  80
56 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat     288
57 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
58             85                  90                  95
60 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc     336
61 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
62             100                 105                 110
```

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Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\06212004\I840277C.raw

```
64 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag       384
65 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
66         115                 120                 125
68 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc       432
69 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
70         130                 135                 140
72 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg       480
73 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
74 145                 150                 155                 160
76 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct       528
77 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
78                 165                 170                 175
80 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc       576
81 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
82                 180                 185                 190
84 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg       624
85 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
86         195                 200                 205
88 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg       672
89 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
90         210                 215                 220
92 tct ccg ggt aaa                                                       684
93 Ser Pro Gly Lys
94 225
```

97 <210> SEQ ID NO: 2
98 <211> LENGTH: 228
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2

```
104 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
105 1               5               10                  15
108 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
109             20                  25                  30
112 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
113         35                  40                  45
116 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
117     50                  55                  60
120 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
121 65                  70                  75                  80
124 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
125                 85                  90                  95
128 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
129             100                 105                 110
132 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
133         115                 120                 125
136 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
137         130                 135                 140
140 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
141 145                 150                 155                 160
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/840,277C**

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Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\06212004\I840277C.raw**

```
144 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
145                165                 170                175
148 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
149                180                 185                190
152 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
153                195                 200                205
156 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
157         210                 215                 220
160 Ser Pro Gly Lys
161 225
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 8
166 <212> TYPE: PRT
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Preferred linker
172 <400> SEQUENCE: 3
174 Gly Gly Gly Lys Gly Gly Gly Gly
175 1               5
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 8
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Preferred linker
186 <400> SEQUENCE: 4
188 Gly Gly Gly Asn Gly Ser Gly Gly
189 1               5
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 8
194 <212> TYPE: PRT
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Preferred linker
200 <400> SEQUENCE: 5
202 Gly Gly Gly Cys Gly Gly Gly Gly
203 1               5
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 5
208 <212> TYPE: PRT
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Preferred linker
214 <400> SEQUENCE: 6
216 Gly Pro Asn Gly Gly
217 1               5
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 5
222 <212> TYPE: PRT
```

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Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\06212004\I840277C.raw

```
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Laminin peptide
228 <400> SEQUENCE: 7
230 Tyr Ile Gly Ser Arg
231 1               5
234 <210> SEQ ID NO: 8
235 <211> LENGTH: 49
236 <212> TYPE: PRT
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Echistatin peptide
242 <400> SEQUENCE: 8
244 Glu Cys Glu Ser Gly Pro Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu
245 1               5                   10                  15
248 Gly Thr Ile Cys Lys Arg Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys
249             20                  25                  30
252 Asn Gly Lys Thr Cys Asp Cys Pro Arg Asn Pro His Lys Gly Pro Ala
253         35                  40                  45
256 Thr
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 7
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: RGD, NGR derivative peptide
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (2, 5 and)..(7)
272 <223> OTHER INFORMATION: Xaa is any amino acid
274 <400> SEQUENCE: 9
```
W--> 276 Arg Xaa Glu Thr Xaa Trp Xaa
```
277 1               5
280 <210> SEQ ID NO: 10
282 <400> SEQUENCE: 10
```
W--> 283 000
```
285 <210> SEQ ID NO: 11
286 <211> LENGTH: 9
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: RGD, NGR derivative peptide
294 <220> FEATURE:
295 <221> NAME/KEY: misc_feature
296 <222> LOCATION: (2, 3, 7 and)..(8)
297 <223> OTHER INFORMATION: Xaa is any amino acid
299 <400> SEQUENCE: 11
```
W--> 301 Cys Xaa Xaa Arg Leu Asp Xaa Xaa Cys
```
302 1               5
```

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Input Set : A:\A-688A.ST25.txt
Output Set: N:\CRF4\06212004\I840277C.raw

```
     305 <210> SEQ ID NO: 12
     307 <400> SEQUENCE: 12
W--> 308 000
     310 <210> SEQ ID NO: 13
     311 <211> LENGTH: 9
     312 <212> TYPE: PRT
     313 <213> ORGANISM: Artificial Sequence
     315 <220> FEATURE:
     316 <223> OTHER INFORMATION: RGD, NGR derivative peptide
     319 <220> FEATURE:
     320 <221> NAME/KEY: misc_feature
     321 <222> LOCATION: (1, 2, 3, 7, 8 and)..(9)
     322 <223> OTHER INFORMATION: Xaa is any amino acid with Xaa at 1, 3, 7 and 9 capable of
     323       forming a bridge.
     325 <400> SEQUENCE: 13
W--> 327 Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa
     328 1               5
     331 <210> SEQ ID NO: 14
     332 <211> LENGTH: 17
     333 <212> TYPE: PRT
     334 <213> ORGANISM: Artificial Sequence
     336 <220> FEATURE:
     337 <223> OTHER INFORMATION: RGD, NGR derivative peptide
     340 <220> FEATURE:
     341 <221> NAME/KEY: misc_feature
     342 <222> LOCATION: (2, 3, 4, 5, 6, 12, 13, 14, 15 and)..(16)
     343 <223> OTHER INFORMATION: At positions 2, 3, 4, 5, 6, 12, 13, 14, 15 and 16, Xaa is
any
     344       amino acid or may be absent.
     346 <400> SEQUENCE: 14
W--> 348 Cys Xaa Xaa Xaa Xaa Xaa Cys Arg Gly Asp Cys Xaa Xaa Xaa Xaa Xaa
     349 1               5                   10                  15
     352 Cys
     356 <210> SEQ ID NO: 15
     357 <211> LENGTH: 8
     358 <212> TYPE: PRT
     359 <213> ORGANISM: Artificial Sequence
     361 <220> FEATURE:
     362 <223> OTHER INFORMATION: RGD, NGR derivative peptide
     365 <220> FEATURE:
     366 <221> NAME/KEY: misc_feature
     367 <222> LOCATION: (1 and)..(8)
     368 <223> OTHER INFORMATION: Xaa is an independently selected amino acid.
     370 <220> FEATURE:
     371 <221> NAME/KEY: misc_feature
     372 <222> LOCATION: (2 and)..(7)
     373 <223> OTHER INFORMATION: Xaa equals 0 to 4 amino acids, each which is independently
     374       selected.
     376 <220> FEATURE:
     377 <221> NAME/KEY: misc_feature
```

variable length not permitted. See item 5 on Error Summary Sheet.

<222> LOCATION: (4)..(4)   *Asp is at location 4*

<223> OTHER INFORMATION: Xaa is selected from the group consisting of glycine
and leucine.

<220> FEATURE:

<221> NAME/KEY: misc_feature   *what about Xaa at location 6?*

<222> LOCATION: (5)..(5)

<223> OTHER INFORMATION: Xaa is selected from the group consisting of tryptophan
and

leucine.

<400> SEQUENCE: 15

Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa

1   5

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Input Set : **A:\A-688A.ST25.txt**
Output Set: **N:\CRF4\06212004\I840277C.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 2,5,7
Seq#:11; Xaa Pos. 2,3,7,8
Seq#:13; Xaa Pos. 1,2,3,7,8,9
Seq#:14; Xaa Pos. 2,3,4,5,6,12,13,14,15,16
Seq#:15; Xaa Pos. 1,2,5,6,7,8
Seq#:16; Xaa Pos. 1,2,3,6,7,8,9,10
Seq#:17; Xaa Pos. 3,5,6,13,15
Seq#:18; Xaa Pos. 2,3,4,7,15
Seq#:19; Xaa Pos. 3,4,5,6,8,13,15,18
Seq#:20; Xaa Pos. 2,5,6,7,12,13,14
Seq#:21; Xaa Pos. 1,3,6,9,12,13
Seq#:40; Xaa Pos. 3,4
Seq#:50; Xaa Pos. 2,3
Seq#:58; Xaa Pos. 5
Seq#:59; Xaa Pos. 6
Seq#:86; Xaa Pos. 3,15
Seq#:87; Xaa Pos. 13,15

VERIFICATION SUMMARY
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Input Set : **A:\A-688A.ST25.txt**
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```
L:276  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:283  M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:301  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:308  M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:327  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:348  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:389  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:437  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:457  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:481  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:501  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
M:341 Repeated in SeqNo=19
L:525  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:545  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:817  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:963  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
```